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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/900,963	07/10/2001	Claudine Guerin-Marchand	010830-118	8667

21839 7590 04/04/2006

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EXAMINER	
LUCAS, ZACHARIAH	
ART UNIT	**PAPER NUMBER**
1648	

DATE MAILED: 04/04/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER

DATE MAILED:

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Commissioner for Patents

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth below or on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. **Neither the paper copy, nor the computer readable form (CRF) of the sequence listings complies with the sequence rules for the reasons indicated in the attached RAW SEQUENCE LISTING ERROR REPORT.**

Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Zachariah Lucas whose telephone number is 571-272-0905. The examiner can normally be reached on Monday-Friday, 8 am to 4:30 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, James Housel can be reached on 571-272-0902. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Z. Lucas
Patent Examiner 3/31/06

Note- attached Raw Sequence Listing Error Report

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/900,963 B
Source: IFW16
Date Processed by STIC: 12/15/2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses;

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/900,963B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	~~Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.~~ Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFW16

RAW SEQUENCE LISTING DATE: 12/15/2005
PATENT APPLICATION: **US/09/900,963B** TIME: 08:47:31

Input Set : **N:\Crf4\Refhold\09_folder\I900963B.raw**
Output Set: **N:\CRF4\12152005\I900963B.raw**

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      1 <110> APPLICANT: GUERIN-MARCHAND, CLAUDINE
      2       DRUILHE, PIERRE
      3 <120> TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF P.
FALCIPARUM
      4       BEARING EPITOPES CAPABLE OF STIMULATING THE T LYMPHOCYTES
      5 <130> FILE REFERENCE: 010830-118
C-->  6 <140> CURRENT APPLICATION NUMBER: US/09/900,963B
      7 <141> CURRENT FILING DATE: 2001-07-10
      8 <150> PRIOR APPLICATION NUMBER: 08/098,327
      9 <151> PRIOR FILING DATE: 1993-11-24
     10 <150> PRIOR APPLICATION NUMBER: PCT/FR92/00104
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     14 <160> NUMBER OF SEQ ID NOS: 47
     15 <170> SOFTWARE: PatentIn Ver. 3.3
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pp 1-2, 5, 7

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

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    770 <212> TYPE: DNA
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    772 <221> NAME/KEY: CDS
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    777         1               5                  10                  15
    778       ttg ata ttt cat ata aat gga aag ata ata aag aat tct gaa aaa gat  96
    779       Leu Ile Phe His Ile Asn Gly Lys Ile Ile Lys Asn Ser Glu Lys Asp
    780                    20                  25                  30
    781       gaa atc ata aaa tct aac ttg aga agt ggt tct tca aat tct agg aat  144
    782       Glu Ile Ile Lys Ser Asn Leu Arg Ser Gly Ser Ser Asn Ser Arg Asn
    783                35                  40                  45
    784       cga ata aat gag gaa aat cac gag aag aaa cac gtt tta tct cat aat  192
    785       Arg Ile Asn Glu Glu Asn His Glu Lys Lys His Val Leu Ser His Asn
    786             50                  55                  60
    787       tca tat gag aaa act aaa aat aat gaa aat aat aaa ttt ttc gat aag  240
    788       Ser Tyr Glu Lys Thr Lys Asn Asn Glu Asn Asn Lys Phe Phe Asp Lys
    789         65                  70                  75                  80
    790       gat aaa gag tta acg atg tct aat gta aaa aat gtg tca caa aca aat  288
    791       Asp Lys Glu Leu Thr Met Ser Asn Val Lys Asn Val Ser Gln Thr Asn
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Insert C 2207 whenever C2217, C2227 or C2237 is

Sheron C2207 never has a response it is a header only.

RAW SEQUENCE LISTING DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B TIME: 08:47:31

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Output Set: N:\CRF4\12152005\I900963B.raw

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793       ttc aaa agt ctt tta aga aat ctt ggt gtt tca gag aat ata ttc ctt   336
794       Phe Lys Ser Leu Leu Arg Asn Leu Gly Val Ser Glu Asn Ile Phe Leu
795                   100                 105                 110
796       aaa gaa aat aaa tta aat aag gaa ggg aaa tta att gaa cac ata ata   384
797       Lys Glu Asn Lys Leu Asn Lys Glu Gly Lys Leu Ile Glu His Ile Ile
798               115                 120                 125
799       aat gat gat gac gat aaa aaa aaa tat att aaa ggg caa gac gaa aac   432
800       Asn Asp Asp Asp Asp Lys Lys Lys Tyr Ile Lys Gly Gln Asp Glu Asn
801           130                 135                 140
802       aga caa gaa gat ctt gaa gaa aaa gca gct aaa gaa aag tta cag ggg   480
803       Arg Gln Glu Asp Leu Glu Glu Lys Ala Ala Lys Glu Lys Leu Gln Gly
804       145                 150                 155                 160
805       caa caa agc gat tca gaa caa gag aga cgt gct aaa gaa aag ttg caa   528
806       Gln Gln Ser Asp Ser Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln
807                       165                 170                 175
808       gaa caa caa agc gat tta gaa caa gag aga ctt gct aaa gaa aag ttg   576
809       Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys Glu Lys Leu
810                   180                 185                 190
811       caa gaa caa caa agc gat tta gaa caa gag aga cgt gct aaa gaa aag   624
812       Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys
813               195                 200                 205
814       ttg caa gaa caa caa agc gat tta gaa caa gag aga ctt gct aaa gaa   672
815       Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys Glu
816           210                 215                 220
817       aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt gct aaa   720
818       Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys
819       225                 230                 235                 240
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821       Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
822                       245                 250                 255
823       aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga ctt   816
824       Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu
825                   260                 265                 270
826       gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gat aga   864
827       Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
828               275                 280                 285
829       ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag   912
830       Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
831           290                 295                 300
832       aga cgt gct aaa gaa agg ttg caa gaa caa caa agc gat tta           954
833       Arg Arg Ala Lys Glu Arg Leu Gln Glu Gln Gln Ser Asp Leu
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928 <211> LENGTH: 1494
929 <212> TYPE: DNA
930 <213> ORGANISM: Plasmodium falciparum
931 <221> NAME/KEY: CDS
932 <222> LOCATION: (1)..(1494)
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RAW SEQUENCE LISTING DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B TIME: 08:47:31

Input Set : N:\Crf4\Refhold\09_folder\I900963B.raw
Output Set: N:\CRF4\12152005\I900963B.raw

E--> 933 <400> SEQUENCE: 42

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934  caa gaa caa caa agc gat cta gaa caa gag aga cgt gct aaa gaa aag   48
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936    1               5                  10                  15
937  ttg caa gaa caa caa agc gat tta gaa caa gat aga ctt gct aaa gaa   96
938  Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu
939                 20                  25                  30
940  aag tta caa gag cag caa agc gat tta gaa caa gag aga ctt gct aaa   144
941  Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys
942             35                  40                  45
943  gaa aag ttg caa gaa caa caa agc gat cta gaa caa gag aga cgt gct   192
944  Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
945         50                  55                  60
946  aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt   240
947  Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg
948    65                  70                  75                  80
949  gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gat aga   288
950  Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
951                     85                  90                  95
952  ctt gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gag   336
953  Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
954                 100                 105                 110
955  aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa   384
956  Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln
957             115                 120                 125
958  gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa   432
959  Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu
960         130                 135                 140
961  caa gag aga ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta   480
962  Gln Glu Arg Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu
963  145                 150                 155                 160
964  gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat   528
965  Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp
966                     165                 170                 175
967  tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc   576
968  Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser
969                 180                 185                 190
970  gat tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gag cag caa   624
971  Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln
972             195                 200                 205
973  aga gat tta gaa caa agg aag gct gat acg aaa aaa aat tta gaa aga   672
974  Arg Asp Leu Glu Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg
975         210                 215                 220
976  aaa aag gaa cat gga gat ata tta gca gag gat tta tat ggt cgt tta   720
977  Lys Lys Glu His Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu
978  225                 230                 235                 240
979  gaa ata cca gct ata gaa ctt cca tca gaa aat gaa cgt gga tat tat   768
980  Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr
981                     245                 250                 255
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RAW SEQUENCE LISTING DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B TIME: 08:47:31

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982       ata cca cat caa tct tct tta cct cag gac aac aga ggg aat agt aga   816
983       Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg
984                260                 265                 270
985       gat tcc aag gaa ata tct ata ata gaa aaa aca aat aga gaa tct att   864
986       Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile
987            275                 280                 285
988       aca aca aat gtt gaa gga cga agg gat ata cat aaa gga cat ctt gaa   912
989       Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu
990        290                 295                 300
991       gaa aag aaa gat ggt tca ata aaa cca gaa caa aaa gaa gat aaa tct   960
992       Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser
993       305                 310                 315                 320
994       gct gac ata caa aat cat aca tta gag aca gta aat att tct gat gtt   1008
995       Ala Asp Ile Gln Asn His Thr Leu Glu Thr Val Asn Ile Ser Asp Val
996                      325                 330                 335
997       aat gat ttt caa ata agt aag tat gag gat gaa ata agt gct gaa tat   1056
998       Asn Asp Phe Gln Ile Ser Lys Tyr Glu Asp Glu Ile Ser Ala Glu Tyr
999                340                 345                 350
1000       gac gat tca tta ata gat gaa gaa gaa gat gat gaa gac tta gac gaa   1104
1001       Asp Asp Ser Leu Ile Asp Glu Glu Glu Asp Asp Glu Asp Leu Asp Glu
1002            355                 360                 365
1003       ttt aag cct att gtg caa tat gac aat ttc caa gat gaa gaa aac ata   1152
1004       Phe Lys Pro Ile Val Gln Tyr Asp Asn Phe Gln Asp Glu Glu Asn Ile
1005           370                 375                 380
1006       gga att tat aaa gaa cta gaa gat ttg ata gag aaa aat gaa aat tta   1200
1007       Gly Ile Tyr Lys Glu Leu Glu Asp Leu Ile Glu Lys Asn Glu Asn Leu
1008       385                 390                 395                 400
1009       gat gat tta gat gaa gga ata gaa aaa tca tca gaa gaa tta tct gaa   1248
1010       Asp Asp Leu Asp Glu Gly Ile Glu Lys Ser Ser Glu Glu Leu Ser Glu
1011                     405                 410                 415
1012       gaa aaa ata aaa aaa gga aag aaa tat gaa aaa aca aag gat aat aat   1296
1013       Glu Lys Ile Lys Lys Gly Lys Lys Tyr Glu Lys Thr Lys Asp Asn Asn
1014                420                 425                 430
1015       ttt aaa cca aat gat aaa agt ttg tat gat gag cat att aaa aaa tat   1344
1016       Phe Lys Pro Asn Asp Lys Ser Leu Tyr Asp Glu His Ile Lys Lys Tyr
1017             435                 440                 445
1018       aaa aat gat aag cag gtt aat aag gaa aag gaa aaa ttc ata aaa tca   1392
1019       Lys Asn Asp Lys Gln Val Asn Lys Glu Lys Glu Lys Phe Ile Lys Ser
1020           450                 455                 460
1021       ttg ttt cat ata ttt gac gga gac aat gaa att tta cag atc gtg gat   1440
1022       Leu Phe His Ile Phe Asp Gly Asp Asn Glu Ile Leu Gln Ile Val Asp
1023       465                 470                 475                 480
1024       gag tta tct gaa gat ata act aaa tat ttt atg aaa cta taa aag gtt   1488
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1112 <211> LENGTH: 1494
1113 <212> TYPE: DNA
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RAW SEQUENCE LISTING DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B TIME: 08:47:31

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Output Set: N:\CRF4\12152005\I900963B.raw

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1114 <213> ORGANISM: Plasmodium falciparum
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1116 <222> LOCATION: (1)..(1494)
E--> 1117 <400> SEQUENCE: 46

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1120        1               5                  10                  15
1121       ttg caa gaa caa caa agc gat tta gaa caa gat aga ctt gct aaa gaa   96
1122       Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu
1123                   20                  25                  30
1124       aag tta caa gag cag caa agc gat tta gaa caa gag aga ctt gct aaa   144
1125       Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys
1126                35                  40                  45
1127       gaa aag ttg caa gaa caa caa agc gat cta gaa caa gag aga cgt gct   192
1128       Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
1129            50                  55                  60
1130       aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt   240
1131       Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg
1132        65                  70                  75                  80
1133       gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gat aga   288
1134       Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
1135                       85                  90                  95
1136       ctt gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gag   336
1137       Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
1138                   100                 105                 110
1139       aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa   384
1140       Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln
1141               115                 120                 125
1142       gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa   432
1143       Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu
1144           130                 135                 140
1145       caa gag aga ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta   480
1146       Gln Glu Arg Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu
1147       145                 150                 155                 160
1148       gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat   528
1149       Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp
1150                       165                 170                 175
1151       tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc   576
1152       Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser
1153                   180                 185                 190
1154       gat tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gag cag caa   624
1155       Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln
1156               195                 200                 205
1157       aga gat tta gaa caa agg aag gct gat acg aaa aaa aat tta gaa aga   672
1158       Arg Asp Leu Glu Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg
1159           210                 215                 220
1160       aaa aag gaa cat gga gat ata tta gca gag gat tta tat ggt cgt tta   720
1161       Lys Lys Glu His Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu
1162       225                 230                 235                 240
```

RAW SEQUENCE LISTING DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B TIME: 08:47:31

Input Set : N:\Crf4\Refhold\09_folder\I900963B.raw
Output Set: N:\CRF4\12152005\I900963B.raw

```
1163      gaa ata cca gct ata gaa ctt cca tca gaa aat gaa cgt gga tat tat   768
1164      Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr
1165                  245                 250                 255
1166      ata cca cat caa tct tct tta cct cag gac aac aga ggg aat agt aga   816
1167      Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg
1168              260                 265                 270
1169      gat tcc aag gaa ata tct ata ata gaa aaa aca aat aga gaa tct att   864
1170      Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile
1171          275                 280                 285
1172      aca aca aat gtt gaa gga cga agg gat ata cat aaa gga cat ctt gaa   912
1173      Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu
1174      290                 295                 300
1175      gaa aag aaa gat ggt tca ata aaa cca gaa caa aaa gaa gat aaa tct   960
1176      Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser
1177      305                 310                 315                 320
1178      gct gac ata caa aat cat aca tta gag aca gta aat att tct gat gtt  1008
1179      Ala Asp Ile Gln Asn His Thr Leu Glu Thr Val Asn Ile Ser Asp Val
1180                  325                 330                 335
1181      aat gat ttt caa ata agt aag tat gag gat gaa ata agt gct gaa tat  1056
1182      Asn Asp Phe Gln Ile Ser Lys Tyr Glu Asp Glu Ile Ser Ala Glu Tyr
1183              340                 345                 350
1184      gac gat tca tta ata gat gaa gaa gaa gat gat gaa gac tta gac gaa  1104
1185      Asp Asp Ser Leu Ile Asp Glu Glu Glu Asp Asp Glu Asp Leu Asp Glu
1186          355                 360                 365
1187      ttt aag cct att gtg caa tat gac aat ttc caa gat gaa gaa aac ata  1152
1188      Phe Lys Pro Ile Val Gln Tyr Asp Asn Phe Gln Asp Glu Glu Asn Ile
1189      370                 375                 380
1190      gga att tat aaa gaa cta gaa gat ttg ata gag aaa aat gaa aat tta  1200
1191      Gly Ile Tyr Lys Glu Leu Glu Asp Leu Ile Glu Lys Asn Glu Asn Leu
1192      385                 390                 395                 400
1193      gat gat tta gat gaa gga ata gaa aaa tca tca gaa gaa tta tct gaa  1248
1194      Asp Asp Leu Asp Glu Gly Ile Glu Lys Ser Ser Glu Glu Leu Ser Glu
1195                  405                 410                 415
1196      gaa aaa ata aaa aaa gga aag aaa tat gaa aaa aca aag gat aat aat  1296
1197      Glu Lys Ile Lys Lys Gly Lys Lys Tyr Glu Lys Thr Lys Asp Asn Asn
1198              420                 425                 430
1199      ttt aaa cca aat gat aaa agt ttg tat gat gag cat att aaa aaa tat  1344
1200      Phe Lys Pro Asn Asp Lys Ser Leu Tyr Asp Glu His Ile Lys Lys Tyr
1201          435                 440                 445
1202      aaa aat gat aag cag gtt aat aag gaa aag gaa aaa ttc ata aaa tca  1392
1203      Lys Asn Asp Lys Gln Val Asn Lys Glu Lys Glu Lys Phe Ile Lys Ser
1204      450                 455                 460
1205      ttg ttt cat ata ttt gac gga gac aat gaa att tta cag atc gtg gat  1440
1206      Leu Phe His Ile Phe Asp Gly Asp Asn Glu Ile Leu Gln Ile Val Asp
1207      465                 470                 475                 480
1208      gag tta tct gaa gat ata act aaa tat ttt atg aaa cta taa aag gtt  1488
1209      Glu Leu Ser Glu Asp Ile Thr Lys Tyr Phe Met Lys Leu
1210                  485                 490
1211      ata tat                                                         1494
```

<210> 1
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Formula Sequence

<220>
<221> VARIANT
<222> 8
<223> Xaa = Glu or Gly

<400> 1
Leu Ala Lys Glu Lys Leu Gln Xaa Gln Gln Ser Asp Leu Glu Gln Glu
1 5 10 15
Arg

Insufficient Explanation. Give Source(s) of genetic material (See Item 11 on Error Summary Sheet).

The above is an Example of Global Error

F41

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <225> fields of each sequence using n or Xaa.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B TIME: 08:47:32

Input Set : N:\Crf4\Refhold\09_folder\I900963B.raw
Output Set: N:\CRF4\12152005\I900963B.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3

VERIFICATION SUMMARY DATE: 12/15/2005
PATENT APPLICATION: **US/09/900,963B** TIME: 08:47:32

Input Set : **N:\Crf4\Refhold\09_folder\I900963B.raw**
Output Set: **N:\CRF4\12152005\I900963B.raw**

L:6 M:270 C: Current Application Number differs, Wrong Format
L:28 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:38 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:16
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:16
L:774 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:37
L:933 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:42
L:1117 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:46